



SEQUENCE LISTING

<110 Miller, Brian S.
SHETTY, Jayarama K.

<120> Modified Forms of Pullulanase

<130> GC396-2

~~<140> 09/262,126
<141> 1999-03-03~~

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2794

<212> DNA

<213> B. deramificans

<400> 1

gatgggaaca cgacaacgat cattgtccac tattttgcc ctgctggta ttatcaacct
tggagtctat ggatgtggcc aaaagacgga ggtgggctg aatacgattt caatcaaccg
gctgactctt ttggagctgt tgcaagtgt gatattccag gaaacccaag tcaggttagga
attatcgttc gcactcaaga ttggaccaaa gatgtgagcc ctgaccgcta catagattta
agcaaaggaa atgaggtgtg gctttagaa ggaaacagcc aaattttta taatgaaaaa
gatgctgagg atgcagctaa acccgctgtg agcaacgctt atttagatgc ttcaaaccag
gtgctggta aacttagcca gccgttaact ctggggaa gnnnaagcgg cttagcggt
catgacgaca cagcaaataa ggatattcca gtgacatctg tgaaggatgc aagtcttgt
caagatgtaa ccgctgtttt ggcaggatacc ttccaaacata ttttggagg ttccgattgg
gcacctgata atcacagtac ttattaaaaa aaggtgacta acaatctcta tcaattctca
ggagatctt ctagaggaaa ctaccaatat aaagtggott taaatgatag ctgaaataat
ccgagttacc catctgacaa cattaattt acagtcctg cccgggtgc acacgtca
tttcgtata ttccgtccac tcatgcagtc tatgacacaa ttaataatcc taatgcggat
ttacaagtag aaagcggggt taaaacggat ctgcgtacgg ttactctagg ggaagatcca
gatgtgagcc atactctgtc cattcaaaca gatggctatc aggcaaaagca ggtgataacct
cgtaatgtgc ttaattcattc acagtaatc tattcaggag atgatcttgg gaataacctat
acacagaaaag caacaacctt taaagtctgg gcaccaactt ctactcaagt aaatgttctt
ctttatgaca gtgcaacggg ttctgtaaaca aaaatcgatc ctatgacggc atcgggcat
ggtgtgtggg aagcaacggt taatcaaaac ctgtaaaatt ggtattacat gtatgaggt
acaggccaag gctctaccccg aacggctgtt gatcctttag caactgcgt tgacccaaat
ggaacgagag gcatgattgt ggacctggct aaaacagatc ctgctggctg gaacagtgt
aaacatatta cgccaaagaa tatagaagat gaggtcatct atgaaatgga ttccgtgac
tttccattt accctaattt gggtatgaaa aataaaggga agtatttggc tttacagaa
aaaggaacaa agggccctga caacgtaaag acggggatag attccttaaa acaacttggg
attactcatg tttagcttat gcctgtttc gcatctaaca gtgtcgatga aactgatcca
acccaagata attggggta tgaccctcg aactatgatg ttccctgaagg gcagtgatgt
acaaatgcga atggtaatgc tcgtataaaa gagttttaagg aaatggttct ttcactcgat
cgtgaacaca ttggggtaa catggatgtt gtctataatc ataccttgc cacgcaaaatc
tctgacttcg ataaaattgt accagaatat tattaccgta cgatgatcca ggttaattata
ccaaacggatc aggtactgga aatgaaattt cangcngaaa ggccaatggt tcaaaaattt
attattgatt cccttaagta ttgggtcaat gagttatcata ttgacggctt cgggtttgac
ttaatggcgc tgcttggaaa agacacgatc tccaaagctg cctcggagct tcatgctatt
aatccaggaa ttgcacttta cggtgagcca tggacgggtg gaacctctgc actgcccagat
gatcagcttc tgacaaaagg agctaaaaaa ggcacggggag tagcgggtt taatgacaat
2040

ttacgaaacg cggtggacgg caatgtctt gattcttccg ctcagaaggtt tgcgacagg 2100
gcaacaggt taactgatgc aattaagaat ggcttgagg ggagtattaa tgactttacc 2160
tcttcaccag gtgagacaat taactatgtc acaagtcatg ataactacac cctttgggac 2220
aaaatagccc taagcaatcc taatgattcc gaagcggatc ggattaaaat ggatgaactc 2280
gcacaaggcag ttgttatgac ctcacaaggc gttccattca tgcaaggcgg ggaagaaatg 2340
cttcgttanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcgt caatgagtt 2400
gattggagca ggaagctca atatccagat gtttcaact attatagcgg gctaatccac 2460
cttcgtctg atcacccagc ctccgcattg acgacagcta atgaaatcaa tagccaccc 2520
caattcctaa atagccaga gaacacagtgc ctttatgaaat taactgatca tttataaaa 2580
gacaaatggg gaaatatcat ttttttat aacccaaata aaactgttagc aaccatcaat 2640
ttgcccggcg ggaatgggc aatcaatgct acgagcggta aggtaggaga atccaccctt 2700
ggtaagcagcag agggaaatgtt ccaagtacca ggtatatcta tttatgtatcct tcatcaagag 2760
gtaagcccg accacggtaa aaagtaatag aaaa 2794

*Sab
37*
<210> 2
<211> 958
<212> PRT
<213> B. deramificans

<220>
<221> VARIANT
<222> (1)...(956)
<223> Xaa = Any Amino Acid

<220>
<221> VARIANT
<222> (957)...(957)
<223> Xaa = gap of indeterminate length

<400> 2
Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
1 5 10 15
Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
20 25 30
Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
35 40 45
Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr
50 55 60
Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
65 70 75 80
Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
85 90 95
Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
100 105 110
Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
115 120 125
Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
130 135 140
Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
145 150 155 160
Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
165 170 175
Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val
180 185 190
Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
195 200 205
Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Val Thr Asn Asn

210	215	220													
Leu	Tyr	Gln	Phe	Ser	Gly	Asp	Leu	Pro	Glu	Gly	Asn	Tyr	Gln	Tyr	Lys
225					230				235				240		
Val	Ala	Leu	Asn	Asp	Ser	Trp	Asn	Asn	Ser	Tyr	Pro	Ser	Asp	Asn	Ile
					245				250				255		
Asn	Leu	Thr	Val	Pro	Ala	Gly	Gly	Ala	His	Val	Thr	Phe	Ser	Tyr	Ile
					260				265			270			
Pro	Ser	Thr	His	Ala	Val	Tyr	Asp	Thr	Ile	Asn	Asn	Pro	Asn	Ala	Asp
					275				280			285			
Leu	Gln	Val	Glu	Ser	Gly	Val	Lys	Thr	Asp	Leu	Val	Thr	Val	Thr	Leu
					290				295			300			
Gly	Glu	Asp	Pro	Asp	Val	Ser	His	Thr	Leu	Ser	Ile	Gln	Thr	Asp	Gly
305					310					315			320		
Tyr	Gln	Ala	Lys	Gln	Val	Ile	Pro	Arg	Asn	Val	Leu	Asn	Ser	Ser	Gln
					325					330			335		
Tyr	Tyr	Tyr	Ser	Gly	Asp	Asp	Leu	Gly	Asn	Thr	Tyr	Thr	Gln	Lys	Ala
					340				345			350			
Thr	Thr	Phe	Lys	Val	Trp	Ala	Pro	Thr	Ser	Thr	Gln	Val	Asn	Val	Leu
					355				360			365			
Leu	Tyr	Asp	Ser	Ala	Thr	Gly	Ser	Val	Thr	Lys	Ile	Val	Pro	Met	Thr
					370				375			380			
Ala	Ser	Gly	His	Gly	Val	Trp	Glu	Ala	Thr	Val	Asn	Gln	Asn	Leu	Glu
385					390					395			400		
Asn	Trp	Tyr	Tyr	Met	Tyr	Glu	Val	Thr	Gly	Gln	Gly	Ser	Thr	Arg	Thr
					405					410			415		
Ala	Val	Asp	Pro	Tyr	Ala	Thr	Ala	Ile	Ala	Pro	Asn	Gly	Thr	Arg	Gly
					420					425			430		
Met	Ile	Val	Asp	Leu	Ala	Lys	Thr	Asp	Pro	Ala	Gly	Trp	Asn	Ser	Asp
					435					440			445		
Lys	His	Ile	Thr	Pro	Lys	Asn	Ile	Glu	Asp	Glu	Val	Ile	Tyr	Glu	Met
					450					455			460		
Asp	Val	Arg	Asp	Phe	Ser	Ile	Asp	Pro	Asn	Ser	Gly	Met	Lys	Asn	Lys
465					470					475			480		
Gly	Lys	Tyr	Leu	Ala	Leu	Thr	Glu	Lys	Gly	Thr	Lys	Gly	Pro	Asp	Asn
					485					490			495		
Val	Lys	Thr	Gly	Ile	Asp	Ser	Leu	Lys	Gln	Leu	Gly	Ile	Thr	His	Val
					500					505			510		
Gln	Leu	Met	Pro	Val	Phe	Ala	Ser	Asn	Ser	Val	Asp	Glu	Thr	Asp	Pro
					515					520			525		
Thr	Gln	Asp	Asn	Trp	Gly	Tyr	Asp	Pro	Arg	Asn	Tyr	Asp	Val	Pro	Glu
					530					535			540		
Gly	Gln	Tyr	Ala	Thr	Asn	Ala	Asn	Gly	Asn	Ala	Arg	Ile	Lys	Glu	Phe
545					550					555			560		
Lys	Glu	Met	Val	Leu	Ser	Leu	His	Arg	Glu	His	Ile	Gly	Val	Asn	Met
					565					570			575		
Asp	Val	Val	Tyr	Asn	His	Thr	Phe	Ala	Thr	Gln	Ile	Ser	Asp	Phe	Asp
					580					585			590		
Lys	Ile	Val	Pro	Glu	Tyr	Tyr	Arg	Thr	Met	Ile	Gln	Val	Ile	Ile	
					595					600			605		
Pro	Thr	Asp	Gln	Val	Leu	Glu	Met	Lys	Leu	Xaa	Ala	Glu	Arg	Pro	Met
					610					615			620		
Val	Gln	Lys	Phe	Ile	Ile	Asp	Ser	Leu	Lys	Tyr	Trp	Val	Asn	Glu	Tyr
625					630					635			640		
His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Met	Ala	Leu	Leu	Gly	Lys	Asp
					645					650			655		
Thr	Met	Ser	Lys	Ala	Ala	Ser	Glu	Leu	His	Ala	Ile	Asn	Pro	Gly	Ile
					660					665			670		

Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
 675 680 685
 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
 690 695 700
 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
 705 710 715 720
 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
 725 730 735
 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
 740 745 750
 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
 755 760 765
 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
 770 775 780
 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
 785 790 795 800
 Phe Met Gln Gly Gly Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
 805 810 815
 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
 820 825 830
 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
 835 840 845
 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
 850 855 860
 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
 865 870 875 880
 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
 885 890 895
 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
 900 905 910
 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
 915 920 925
 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
 930 935 940
 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys Xaa Lys
 945 950 955

<210> 3
 <211> 718
 <212> PRT
 <213> B. subtilis

<400> 3

Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
 1 5 10 15
 Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
 20 25 30
 Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
 35 40 45
 Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
 50 55 60
 His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
 65 70 75 80
 His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
 85 90 95
 Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
 100 105 110

Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
 115 120 125
 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
 130 135 140
 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
 145 150 155 160
 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
 165 170 175
 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
 180 185 190
 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
 195 200 205
 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
 210 215 220
 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
 225 230 235 240
 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Gly
 245 250 255
 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
 260 265 270
 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
 275 280 285
 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
 290 295 300
 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
 305 310 315 320
 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
 325 330 335
 Val Phe Asn His Val Tyr Lys Arg Glu Asn Ser Pro Phe Glu Lys Thr
 340 345 350
 Val Pro Gly Tyr Phe Phe Arg His Asp Glu Cys Gly Met Pro Ser Asn
 355 360 365
 Gly Thr Gly Val Gly Asn Asp Ile Ala Ser Glu Arg Arg Met Ala Arg
 370 375 380
 Lys Phe Ile Ala Asp Cys Val Val Tyr Trp Leu Glu Glu Tyr Asn Val
 385 390 395 400
 Asp Gly Phe Arg Phe Asp Leu Leu Gly Ile Leu Asp Ile Asp Thr Val
 405 410 415
 Leu Tyr Met Lys Glu Lys Ala Thr Lys Ala Lys Pro Gly Ile Leu Leu
 420 425 430
 Phe Gly Glu Gly Trp Asp Leu Ala Thr Pro Leu Pro His Glu Gln Lys
 435 440 445
 Ala Ala Leu Ala Asn Ala Pro Arg Met Pro Gly Ile Gly Phe Phe Asn
 450 455 460
 Asp Met Phe Arg Asp Ala Val Lys Gly Asn Thr Phe His Leu Lys Ala
 465 470 475 480
 Thr Gly Phe Ala Leu Gly Asn Gly Glu Ser Ala Gln Ala Val Met His
 485 490 495
 Gly Ile Ala Gly Ser Ser Gly Trp Lys Ala Leu Ala Pro Ile Val Pro
 500 505 510
 Glu Pro Ser Gln Ser Ile Asn Tyr Val Glu Ser His Asp Asn His Thr
 515 520 525
 Phe Trp Asp Lys Met Ser Phe Ala Leu Pro Gln Glu Asn Asp Ser Arg
 530 535 540
 Lys Arg Ser Arg Gln Arg Leu Ala Val Ala Ile Ile Leu Leu Ala Gln
 545 550 555 560
 Gly Val Pro Phe Ile His Ser Gly Gln Glu Phe Phe Arg Thr Lys Gln

565	570	575
Gly Val Glu Asn Ser Tyr Gln Ser Ser Asp Ser Ile Asn Gln Leu Asp		
580	585	590
Trp Asp Arg Arg Glu Thr Phe Lys Glu Asp Val His Tyr Ile Arg Arg		
595	600	605
Leu Ile Ser Leu Arg Lys Ala His Pro Ala Phe Arg Leu Arg Ser Ala		
610	615	620
Ala Asp Ile Gln Arg His Leu Glu Cys Leu Thr Leu Lys Glu His Leu		
625	630	640
Ile Ala Tyr Arg Leu Tyr Asp Leu Asp Glu Val Asp Glu Trp Lys Asp		
645	650	655
Ile Ile Val Ile His His Ala Ser Pro Asp Ser Val Glu Trp Arg Leu		
660	665	670
Pro Asn Asp Ile Pro Tyr Arg Leu Leu Cys Asp Pro Ser Gly Phe Gln		
675	680	685
Glu Asp Pro Thr Glu Ile Lys Lys Thr Val Ala Val Asn Gly Ile Gly		
690	695	700
Thr Val Ile Leu Tyr Leu Ala Ser Asp Leu Lys Ser Phe Ala		
705	710	715

<210> 4

<211> 1091

<212> PRT

<213> K. pneumonia

<400> 4			
Met Leu Arg Tyr Thr Arg Asn Ala Leu Val Leu Gly Ser Leu Val Leu			
1	5	10	15
Leu Ser Gly Cys Asp Asn Gly Ser Ser Ser Ser Ser Ser Gly Asn			
20	25	30	
Pro Asp Thr Pro Asp Asn Gln Asp Val Val Val Arg Leu Pro Asp Val			
35	40	45	
Ala Val Pro Gly Glu Ala Val Thr Ala Val Glu Asn Gln Ala Val Ile			
50	55	60	
His Leu Val Asp Ile Ala Gly Ile Thr Ser Ser Ala Ala Asp Tyr			
65	70	75	80
Ser Ser Lys Asn Leu Tyr Leu Trp Asn Asn Glu Thr Cys Asp Ala Leu			
85	90	95	
Ser Ala Pro Val Ala Asp Trp Asn Asp Val Ser Thr Thr Pro Ser Gly			
100	105	110	
Ser Asp Lys Tyr Gly Pro Tyr Trp Val Ile Pro Leu Asn Lys Glu Ser			
115	120	125	
Gly Cys Ile Asn Val Ile Val Arg Asp Gly Thr Asp Lys Leu Ile Asp			
130	135	140	
Ser Asp Leu Arg Val Ala Phe Gly Asp Phe Thr Asp Arg Thr Val Ser			
145	150	155	160
Val Ile Ala Gly Asn Ser Ala Val Tyr Asp Ser Arg Ala Asp Ala Phe			
165	170	175	
Arg Ala Ala Phe Gly Val Ala Leu Ala Glu Ala His Trp Val Asp Lys			
180	185	190	
Asn Thr Leu Leu Trp Pro Gly Gly Gln Asp Lys Pro Ile Val Arg Leu			
195	200	205	
Tyr Tyr Ser His Ser Ser Lys Val Ala Ala Asp Gly Glu Gly Lys Phe			
210	215	220	
Thr Asp Arg Tyr Leu Lys Leu Thr Pro Thr Thr Val Ser Gln Gln Val			
225	230	235	240
Ser Met Arg Phe Pro His Leu Ser Ser Tyr Ala Ala Phe Lys Leu Pro			

245	250	255
Asp Asn Ala Asn Val Asp Glu Leu Leu Gln Gly Glu Thr Val Ala Ile		
260	265	270
Ala Ala Ala Glu Asp Gly Ile Leu Ile Ser Ala Thr Gln Val Gln Thr		
275	280	285
Ala Gly Val Leu Asp Asp Ala Tyr Ala Glu Ala Ala Glu Ala Leu Ser		
290	295	300
Tyr Gly Ala Gln Leu Ala Asp Gly Gly Val Thr Phe Arg Val Trp Ala		
305	310	315
Pro Thr Ala Gln Gln Val Asp Val Val Val Tyr Ser Ala Asp Lys Lys		
325	330	335
Val Ile Gly Ser His Pro Met Thr Arg Asp Ser Ala Ser Gly Ala Trp		
340	345	350
Ser Trp Gln Gly Gly Ser Asp Leu Lys Gly Ala Phe Tyr Arg Tyr Ala		
355	360	365
Met Thr Val Tyr His Pro Gln Ser Arg Lys Val Glu Gln Tyr Glu Val		
370	375	380
Thr Asp Pro Tyr Ala His Ser Leu Ser Thr Asn Ser Glu Tyr Ser Gln		
385	390	395
Val Val Asp Leu Asn Asp Ser Ala Leu Lys Pro Asp Gly Trp Asp Asn		
405	410	415
Leu Thr Met Pro His Ala Gln Lys Thr Lys Ala Asp Leu Ala Lys Met		
420	425	430
Thr Ile His Glu Ser His Ile Arg Asp Leu Ser Ala Trp Asp Gln Thr		
435	440	445
Val Pro Ala Glu Leu Arg Gly Lys Tyr Leu Ala Leu Thr Ala Gly Asp		
450	455	460
Ser Asn Met Val Gln His Leu Lys Thr Leu Ser Ala Ser Gly Val Thr		
465	470	475
His Val Glu Leu Leu Pro Val Phe Asp Leu Ala Thr Val Asn Glu Phe		
485	490	495
Ser Asp Lys Val Ala Asp Ile Gln Gln Pro Phe Ser Arg Leu Cys Glu		
500	505	510
Val Asn Ser Ala Val Lys Ser Ser Glu Phe Ala Gly Tyr Cys Asp Ser		
515	520	525
Gly Ser Thr Val Glu Glu Val Leu Asn Gln Leu Lys Gln Ser Asp Ser		
530	535	540
Gln Asp Asn Pro Gln Val Gln Ala Leu Asn Thr Leu Val Ala Gln Thr		
545	550	555
Asp Ser Tyr Asn Trp Gly Tyr Asp Pro Phe His Tyr Thr Val Pro Glu		
565	570	575
Gly Ser Tyr Ala Thr Asp Pro Glu Gly Thr Thr Arg Ile Lys Glu Phe		
580	585	590
Arg Thr Met Ile Gln Ala Ile Lys Gln Asp Leu Gly Met Asn Val Ile		
595	600	605
Met Asp Val Val Tyr Asn His Thr Asn Ala Ala Gly Pro Thr Asp Arg		
610	615	620
Thr Ser Val Leu Asp Lys Ile Val Pro Trp Tyr Tyr Gln Arg Leu Asn		
625	630	635
Glu Thr Thr Gly Ser Val Glu Ser Ala Thr Cys Cys Ser Asp Ser Ala		
645	650	655
Pro Glu His Arg Met Phe Ala Lys Leu Ile Ala Asp Ser Leu Ala Val		
660	665	670
Trp Thr Thr Asp Tyr Lys Ile Asp Gly Phe Arg Phe Asp Leu Met Gly		
675	680	685
Tyr His Pro Lys Ala Gln Ile Leu Ser Ala Trp Glu Arg Ile Lys Ala		
690	695	700

Leu Asn Pro Asp Ile Tyr Phe Phe Gly Glu Gly Trp Asp Ser Asn Gln
 705 710 715 720
 Ser Asp Arg Phe Glu Ile Ala Ser Gln Ile Asn Leu Lys Gly Thr Gly
 725 730 735
 Ile Gly Thr Phe Ser Asp Arg Leu Arg Asp Ser Val Arg Gly Gly Gly
 740 745 750
 Pro Phe Asp Ser Gly Asp Ala Leu Arg Gln Asn Gln Gly Ile Gly Ser
 755 760 765
 Gly Ala Gly Val Leu Pro Asn Glu Leu Ala Ser Leu Ser Asp Asp Gln
 770 775 780
 Val Arg His Leu Ala Asp Leu Thr Arg Leu Gly Met Ala Gly Asn Leu
 785 790 795 800
 Ala Asp Phe Val Met Ile Asp Lys Asp Gly Ala Ala Lys Lys Gly Ser
 805 810 815
 Glu Ile Asp Tyr Asn Gly Ala Pro Gly Gly Tyr Ala Ala Asp Pro Thr
 820 825 830
 Glu Val Val Asn Tyr Val Ser Lys His Asp Asn Gln Thr Leu Trp Asp
 835 840 845
 Met Ile Ser Tyr Lys Ala Ser Gln Glu Ala Asp Leu Ala Thr Arg Val
 850 855 860
 Arg Met Gln Ala Val Ser Leu Ala Thr Val Met Leu Gly Gln Gly Ile
 865 870 875 880
 Ala Phe Asp Gln Gln Gly Ser Glu Leu Leu Arg Ser Lys Ser Phe Thr
 885 890 895
 Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Arg Val Asp Tyr Ser
 900 905 910
 Leu Gln Asp Asn Asn Tyr Asn Val Gly Met Pro Arg Ile Ser Asp Asp
 915 920 925
 Gly Ser Asn Tyr Glu Val Ile Thr Arg Val Lys Glu Met Val Ala Thr
 930 935 940
 Pro Gly Glu Ala Glu Leu Lys Gln Met Thr Ala Phe Tyr Gln Glu Leu
 945 950 955 960
 Thr Glu Leu Arg Lys Ser Ser Pro Leu Phe Thr Leu Gly Asp Gly Ser
 965 970 975
 Ala Val Met Lys Arg Val Asp Phe Arg Asn Thr Gly Ser Asp Gln Gln
 980 985 990
 Ala Gly Leu Leu Val Met Thr Val Asp Asp Gly Met Lys Ala Gly Ala
 995 1000 1005
 Ser Leu Asp Ser Arg Leu Asp Gly Leu Val Val Ala Ile Asn Ala Ala
 1010 1015 1020
 Pro Glu Ser Arg Thr Leu Asn Glu Phe Ala Gly Glu Thr Leu Gln Leu
 1025 1030 1035 104
 Ser Ala Ile Gln Gln Thr Ala Gly Glu Asn Ser Leu Ala Asn Gly Val
 1045 1050 1055
 Gln Ile Ala Ala Asp Gly Thr Val Thr Leu Pro Ala Trp Ser Val Ala
 1060 1065 1070
 Val Leu Glu Leu Pro Gln Gly Glu Ala Gln Gly Ala Gly Leu Pro Val
 1075 1080 1085
 Ser Ser Lys
 1090

<210> 5
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Unknown

<400> 5

Asp Val Val Ile Asn His
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown

<400> 6

Gly Phe Arg Leu Asp Ala Ala Lys His
1 5

<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown

<400> 7

Phe Val Asp Val His Asp
1 5

<210> 8

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown

<400> 8

Tyr Asn Trp Gly Tyr
1 5

<210> 9

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown

<400> 9

Val Trp Ala Pro
1